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Comparison of Effects of Antimicrobial Interventions on Multidrug-Resistant *Salmonella,* Susceptible *Salmonella,* and *Escherichia coli* O157:H7†

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ABSTRACT

Several strains of *Salmonella* have been identified as resistant to multiple antibiotics. What is not known is whether strains possessing multidrug resistance properties also have the ability to resist the killing effects of the antimicrobial interventions used in beef processing. The research project described herein was designed to determine whether antimicrobial interventions currently in place in beef processing facilities are adequate for reducing the foodborne pathogen loads on beef carcass surfaces contaminated with multidrug-resistant (MDR) *Salmonella.* The data presented here indicate that MDR *Salmonella* is reduced at least as effectively as are *Escherichia coli* O157:H7 and susceptible *Salmonella* when treated with antimicrobial interventions currently in use at most U.S. beef processing plants. The *E. coli* O157:H7 strains used in this study were divided into two groups, strains that have a genetic polymorphism associated with human disease and strains not typically found to cause human disease. No differences were detected in the abilities of these two strain types to survive antimicrobial interventions. These results indicate that neither the drug resistance status of a particular *Salmonella* strain nor the likelihood that a particular *E. coli* O157:H7 strain will cause human illness influences the antimicrobial efficacy of the interventions utilized by the modern beef processing plants.

Escherichia coli O157:H7 and *Salmonella* are frequently detected in the intestinal tracts and on the hides of cattle *(5).* During processing, these organisms can be transferred to the carcass, and antimicrobial interventions employed in the beef processing plants are then relied upon to kill or remove potential foodborne pathogens to prevent contamination of the finished product *(2).* This reliance on antimicrobial interventions is based on efficacy studies and the belief that similar organisms will be affected by interventions in an similar manner. However, *E. coli* O157:H7 and *Salmonella* populations are heterogeneous with respect to resistance to antimicrobials and the ability to cause disease *(1, 6, 7, 12).*

Recently, antibiotic-resistant organisms have emerged that present challenges to the treatment of clinical disease. Bacteria are constantly acquiring new genetic sequences from other microorganisms and their local environment. These genetic acquisitions have allowed some strains to become resistant to various antibiotics. The transferable DNA coding for resistance to one antibiotic frequently contains genes that code for resistance to additional antibiotics, and the cellular modifications that result from the new genetic material frequently provide protection against specific antimicrobials and other antimicrobials that function through similar mechanisms or at the same sites of action. Several strains of *Salmonella* have been identified as resistant to multiple antibiotics *(1).* These multidrug-resistant (MDR) *Salmonella* strains are viewed as emerging foodborne pathogens. What is not known is whether strains possessing multidrug resistance properties also have the ability to resist the killing effects of the antimicrobial interventions used in beef processing. The research project described herein was designed to determine whether antimicrobial interventions currently in place in beef processing facilities are adequate for reducing the foodborne pathogen loads of beef carcasses contaminated with MDR *Salmonella.*

Recent studies have revealed variation within *E. coli* O157:H7 populations with regard to the ability to cause human disease *(6, 7, 12).* Specific genetic polymorphisms associated with higher incidences of human disease have been identified in *E. coli* O157:H7 strains *(7).* The second objective of this project was to evaluate *E. coli* O157:H7 strains associated with human disease and strains not associated with human disease for their ability to survive antimicrobial interventions.

MATERIALS AND METHODS

Bacterial strains. The bacterial strains utilized in the study are listed in Table 1. The *Salmonella* strains consisted of both *Salmonella* Typhimurium and Newport serotypes with each serotype being further subdivided into MDR and sensitive categories. The *E. coli* O157:H7 strains were subdivided into strains associated with human disease and strains that are not typically found to cause human disease as defined by the *tir* 255 polymor-

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† Mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.

TABLE 1. *Bacterial strains and antibiotic resistance status*

Organism	Type[a]	Strain designation	Antibiotic resistance profile[b]	Source[c]
Salmonella Newport	MDR	13324 POH2	AmApFT(Ax)CSSuTe	USMARC
		13212 PRH2	CKSSuT	USMARC
		13109 PRB1	AmApFTAxCGKSSuTe	USMARC
	Susceptible	15124 PRH2	Not resistant	USMARC
		645 AH1	Not resistant	USMARC
		644 AB2	Not resistant	USMARC
Salmonella Typhimurium	MDR	12246 PRH2	(Am)ApCSSuTe	USMARC
		11241 PRB1	AmApFT(Ax)CKSSuTe	USMARC
		720 AB2	CSSuTe	USMARC
	Susceptible	14218 PRH2	Not resistant	USMARC
		14249 PRB1	Not resistant	USMARC
		14164 PRB1	Not resistant	USMARC
E. coli O157:H7	HDA	43895	ND	ATCC
		EL40164	ND	FSIS
		EL50165	ND	FSIS
	Non-HDA	CO50	ND	USMARC
		SSNE1040	ND	USMARC
		KS368	ND	USMARC

[a] MDR, multidrug resistant; HDA, human disease associated.

[b] Am, amoxicillin–clavulanic acid; Ap, ampicillin; F, cefoxitin; T, ceftiofur; Ax, ceftriaxone; C, chloramphenicol; G, gentamicin; K, kanamycin; S, streptomycin; Su, sulfisoxazole; Te, tetracycline; ND, not determined. Antibiotics in parentheses indicate intermediate resistance (i.e., the MIC was increased but was below the resistance breakpoint).

[c] USMARC, U.S. Meat Animal Research Center (Clay Center, Nebr.); ATCC, American Type Culture Collection (Manassas, Va.); FSIS, Food Safety and Inspection Service (Athens, Ga.).

phism *(7). E. coli* O157:H7, *Salmonella* Newport, and *Salmonella* Typhimurium strains were grown individually for 18 to 24 h at 37°C in tryptic soy broth (TSB; Becton Dickinson, Sparks, Md.). The following morning, 1-ml aliquots of each strain culture were mixed into cocktails by organism type. After mixing, the strain cocktails were diluted in buffered peptone water (Becton Dickinson) to $\sim 1 \times 10^8$ CFU/ml. The diluted cocktails were stored on ice during the experiment.

Flank tissue. Pieces of flank tissue ($\sim$700 cm^2) were collected from beef carcasses at a local processing plant. The tissues (cutaneous trunci muscle) were obtained within 15 min of exsanguination before the carcasses entered the antimicrobial wash cabinet. The tissue sections were transported back to the U.S. Meat Animal Research Center in insulated carriers to prevent rapid cooling. Before inoculation, four 100-cm^2 areas were marked on each flank section with edible ink, a sterile cotton-tipped swab, and a stainless steel 100-cm^2 template. Each 100-cm^2 area was divided into four 25-cm^2 areas. Each 100-cm^2 section was inoculated with 500 μl of a strain cocktail at $\sim 1 \times 10^8$ CFU/ml for a final concentration of $\sim 5 \times 10^5$ CFU/cm^2. Three flanks were used per organism for each treatment, resulting in 12 replications per organism per treatment.

Treatment. After inoculation, the flank sections were incubated for 15 min at room temperature to allow bacterial attachment. After attachment, sections were washed with water (25 ± 2°C) at 45 psi for 10 s to remove any unattached bacteria. Excess water was allowed to drip off for 30 s. After the water wash, the various treatments were applied at 25 psi for 20 s. The treatments consisted of acetic acid (2%; Sigma, St. Louis, Mo.), electrolyzed oxidizing water (acidic, pH 2.8, 60 ppm of chlorine with 1,190 mV of oxidation-reduction potential; Electric Aquagenics, Kennesaw, Ga.), FreshFX (1:50, pH 1.6; SteriFX, Inc., Shreveport, La.), hot water (74°C at the nozzles), DL-lactic acid (2%; Sigma), and ozonated water (6.0 ppm; Ozone International, Bainbridge Island, Wash.). Excess liquid was allowed to drip off for 30 s after each treatment. Treatment sprays were applied in an insertable pod in a laminar air flow hood *(10).* The spray nozzle oscillation speed was 60 cycles per min.

Sampling. From each 100-cm^2 section, two 25-cm^2 pieces of surface tissue were excised; one was removed after the water wash and the other was removed after the treatment. Each 25-cm^2 section was placed in a sterile Whirl-Pak bag (Nasco, Ft. Atkinson, Wis.).

Sample processing. Each bag received 25 ml of TSB-PO_4 (TSB supplemented with 0.017 M KH_2PO_4 and 0.072 M K_2HPO_4 [Sigma], pH 7.2 ± 0.1), and the bag contents were homogenized for 1 min at 9 strokes per s (540 rpm) with a homogenizer (BagMixer 400, Interscience, Weymouth, Mass.). After homogenization, the sample contents (50 μl) were serially diluted 10-fold, and the appropriate dilutions were plated with a spiral plater (Spiral Biotech, Norwood, Mass.) onto plates of xylose lysine deoxycholate agar (Oxoid, Basingstoke, UK) and ntChromagar (CHROMAgar O157, DRG International, Mountainside, N.J.) supplemented with 5 mg/liter novobiocin and 1.0 mg/liter of potassium tellurite. Plates were incubated for 18 to 20 h at 37°C. All colonies were counted manually, and colony counts were log transformed for analysis.

Statistical analysis. Each antimicrobial was evaluated in an independent study. Therefore, a separate analysis of variance (ANOVA) was conducted for each antimicrobial to determine whether pathogens (strain within organism combinations) were differentially sensitive to the antimicrobial intervention. Log reduction data were analyzed by one-way ANOVA for a completely randomized design using the Proc GLM procedures of SAS (SAS Institute, Cary, N.C.). Least squares means were separated using

TABLE 2. *Effects of acid treatments on* Escherichia coli *O157:H7 and* Salmonella[a]

Organism	Type[b]	Population reduction (log CFU/cm^2)[c]		
		Acetic acid	Fresh FX	Lactic acid
E. coli O157:H7	HDA	0.65 A	1.49 A	1.47 BC
	Non-HDA	0.65 A	1.55 A	1.15 C
Salmonella Newport	MDR	0.87 A	1.42 A	1.80 A
	Susceptible	0.91 A	0.92 B	1.61 AB
Salmonella Typhimurium	MDR	ND[d]	1.40 A	1.46 BC
	Susceptible	ND	1.24 AB	1.57 AB

[a] Treatments were acetic acid (2%; Sigma, St. Louis, Mo.), FreshFX (1:50, pH 1.6; SteriFX, Inc., Shreveport, La.), and DL-lactic acid (2%; Sigma).
[b] MDR, multidrug resistant; HDA, human disease associated.
[c] Within a treatment, means (average of 12 replications) with a common letter are not significantly different ($P \geq 0.05$).
[d] ND, not determined.

the PDIFF option (a paired *t* test) when the ANOVA was statistically significant. A predetermined probability of type I error (α) of 0.05 was used for all determinations of significance.

RESULTS AND DISCUSSION

Salmonella Typhimurium and *Salmonella* Newport are two of the top three disease-causing *Salmonella* serotypes in the United States and were responsible for 19 and 9%, respectively, of the reported cases of salmonellosis in 2005 *(8).* Salmonellosis can be associated with invasion of extraintestinal lumen tissues and requires antibiotic treatment for recovery. In recent years, there has been a marked increase in the number of MDR *Salmonella* strains isolated in clinical settings. A *Salmonella* Typhimurium strain resistant to five antibiotics and a *Salmonella* Newport strain resistant to nine antibiotics were two of the most common MDR *Salmonella* phenotypes isolated in 2004 *(9).* MDR status in bacteria is generally thought to arise through acquisition of one or more units of extraneous DNA. Bacteria readily acquire new genetic material through a variety of mechanisms (e.g., transformation, transduction, and transposition), and frequently the transferred genetic material codes for resistance to multiple antibiotics *(13).* It has not been determined whether resistance to multiple antibiotics also impacts survivability of these bacteria when they are exposed to antimicrobial interventions used in the meat processing industry.

In the current study, reductions in *E. coli* O157:H7 and *Salmonella* attached to fresh beef tissue surfaces were determined after application of acid (acetic acid, lactic acid, and FreshFX) and nonacid (electrolyzed water, hot water, and ozone) antimicrobial treatments. The experiment described herein was designed to allow a comparison of the survival of the various strain types exposed to a particular antimicrobial intervention and not for comparison of the efficacy of various intervention types among themselves. Hence, these data should not be used as selection criteria for intervention methods.

Of the three acid treatments tested, there were no differences ($P > 0.05$) detected in the ability of various organisms or types to survive when exposed to acetic acid (Table 2). There were differences in survival when the strains were treated with FreshFX and lactic acid. The reductions due to FreshFX treatment were similar ($P > 0.05$) for susceptible *Salmonella* Newport and *Salmonella* Typhimurium. But Fresh FX reduced susceptible *Salmonella* Newport less ($P < 0.05$) than it reduced *E. coli* O157:H7 and MDR *Salmonella.* For lactic acid, all *E. coli* O157:H7 and MDR *Salmonella* Typhimurium reductions were similar ($P > 0.05$), but MDR *Salmonella* Newport was reduced more ($P < 0.05$) than all *E. coli* O157:H7. The other salmonellae had intermediate levels of reduction in response to lactic acid. These results are generally consistent with those reported by Bacon et al. *(4),* in that there was no association between susceptibility to antimicrobial agents and the ability of *Salmonella* strains to survive low pH stress.

When the nonacid treatments were evaluated, no differences ($P > 0.05$) in reductions were detected for *Salmonella* after treatment with ozone (Table 3). The electrolyzed water and hot water treatments both resulted in significant differences in strain survival. Following electrolyzed water treatment, all the *Salmonella* strains were reduced more ($P < 0.05$) than were the *E. coli* O157:H7 human disease–associated (HDA) strains. The electrolyzed water reductions for MDR and susceptible *Salmonella* Typhimurium were not significantly different ($P > 0.05$) from those for the *Salmonella* Newport MDR and susceptible strains but were greater ($P < 0.05$) than those for all *E. coli* O157:H7 strains. Hot water produced the largest magnitude difference in reductions between strains of all of the treatments. After treatment with hot water, the reduction of MDR *Salmonella* Typhimurium was greater than the reductions observed for *Salmonella* Newport or *E. coli* O157:H7, with over a 1-log difference between the reduction of non-HDA *E. coli* O157:H7 and MDR *Salmonella* Typhimurium, and the reduction of MDR *Salmonella* Newport was greater than the reduction of susceptible *Salmonella* Newport. Regardless of antimicrobial treatment, MDR *Salmonella* had similar or greater sensitivity compared with susceptible *Salmonella* or *E. coli* O157:H7.

The results reported herein are in agreement with those reported by Cutter and Rivera-Betancourt *(10),* who found that various antimicrobial treatments (acetic acid, lactic acid, hot water, and trisodium phosphate) were equally ef-

TABLE 3. *Effects of nonacid treatments on* Escherichia coli *O157:H7 and* Salmonella[a]

Organism	Type[b]	Population reduction (log CFU/cm^2)[c]		
		Electrolyzed water	Hot water	Ozone
E. coli O157:H7	HDA	0.30 C	1.26 CD	ND[d]
	Non-HDA	0.46 BC	0.96 D	ND
Salmonella Newport	MDR	0.57 AB	1.53 BC	0.39 A
	Susceptible	0.64 AB	1.04 D	0.23 A
Salmonella Typhimurium	MDR	0.75 A	2.10 A	0.32 A
	Susceptible	0.74 A	1.79 AB	0.35 A

[a] Treatments were electrolyzed water (acidic, pH 2.8, 60 ppm of chlorine with 1,190 mV of oxidation-reduction potential; Electric Aquagenics, Kennesaw, Ga.), hot water (74°C), and ozonated water (6.0 ppm; Ozone International, Bainbridge Island, Wash.).
[b] MDR, multidrug resistant; HDA, human disease associated.
[c] Within a treatment, means (average of 12 replications) with a common letter are not significantly different ($P \geq 0.05$).
[d] ND, not determined.

fective when applied to a susceptible *Salmonella* Typhimurium strain and an antibiotic-resistant *Salmonella* Typhimurium DT104 strain. In that study, only one strain of each type was tested, and *E. coli* O157:H7 was not included. In another study, there was no significant difference in overall heat resistance between MDR and susceptible *Salmonella* strains, although susceptible strains had slightly higher heat resistances at certain temperatures *(16).* Bacon et al. *(3)* also found no difference in the abilities of MDR and susceptible *Salmonella* strains to survive heat stress. Walsh et al. *(17)* reported no difference in thermal resistance between an antibiotic-sensitive *Salmonella* Typhimurium strain and a laboratory-derived antibiotic-resistant strain of *Salmonella* Typhimurium. In the same study, an MDR *Salmonella* Typhimurium DT104 strain isolated from a bovine hide sample had increased thermal resistance, especially following heat shock *(17).* The authors concluded that more data would be needed to rule out interstrain variation, which has been shown to produce differences in thermal tolerance *(11).*

In the current study, *E. coli* O157:H7 was equally or more resistant to the antimicrobial interventions than were the *Salmonella* strains, except for the FreshFX treatment. When FreshFX was applied, susceptible *Salmonella* Newport was reduced less than was *E. coli* O157:H7. Stopforth et al. *(15)* found no difference in the survival of *E. coli* O157:H7 and *Salmonella* when subjected to various antimicrobial interventions (acidified sodium chlorite, chlorine, and acidic electrolyzed water). Whitney et al. *(18)* found that *E. coli* O157:H7 was more resistant to high pressure treatment than was *Salmonella.* Neither of these studies included MDR *Salmonella* strains in their experiments.

No difference was observed in the present study between the HDA and non-HDA strains of *E. coli* O157:H7 in the resistance to antimicrobial interventions. The Shiga toxin-producing *E. coli* O157 *tir* 255 polymorphism used to discriminate the *E. coli* O157:H7 strains in this study has an allele that is overrepresented in the population of HDA isolates *(7).* The *T* allele of this polymorphism was found in 107 (99.1%) of 108 HDA isolates but only 43 (55.8%) of 77 bovine isolates. The researchers hypothesized that an inability to survive antimicrobial interventions may be the reason the non-HDA *E. coli* O157:H7 strains are not found as frequently in human disease cases. The results presented here do not support that hypothesis and indicate that HDA and non-HDA *E. coli* O157:H7 strains survive antimicrobial interventions equally well.

The cell counts reported herein were obtained by plating treated and nontreated cells on selective media. However, cells that had incurred sublethal injury may not have been viable on the selective media and the reductions observed may have overestimated the actual level of cell death resulting from the treatments. Selective media were chosen to reduce the background microflora, which can exceed 5 log CFU/100 cm^2 on preevisceration carcasses *(14).* The reductions observed in this study are in agreement with those in several previously published reports but should be interpreted accordingly.

Information has been lacking as to whether strains possessing multidrug resistance properties or different pathotypes have the ability to resist the killing effects of the antimicrobial interventions used in beef processing. The results of this research indicate that the antimicrobial interventions currently in place in beef processing facilities are equally effective in reducing the foodborne pathogen loads of beef carcasses contaminated with MDR *Salmonella,* susceptible *Salmonella,* and various *E. coli* O157:H7 pathotypes.

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